Full wwPDB X-ray Structure Validation Report (i)

Sep 26, 2023 – 04:30 AM EDT

PDB ID	:	6AZS
Title	:	Structural and biochemical characterization of a non-canonical biuret hydrolase (BiuH) from the cyanuric acid catabolism pathway of Rhizobium leguminasorum bv. viciae 3841
Authors	:	Peat, T.S.; Esquirol, L.; Newman, J.; Scott, C.
Deposited on	:	2017-09-11
Resolution	:	1.59 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

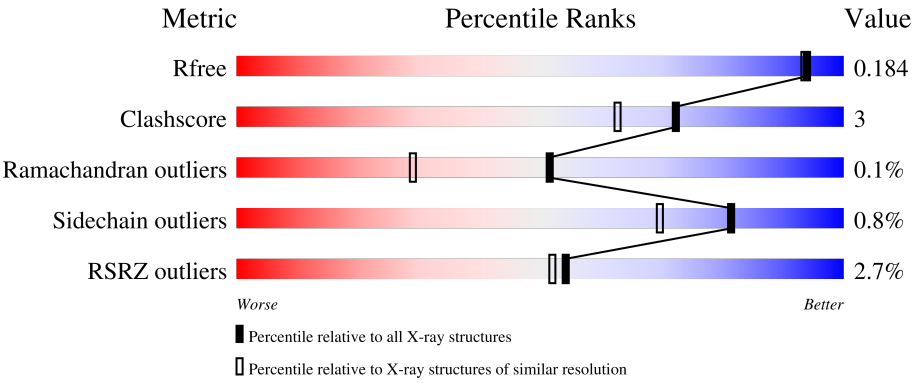
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	262	4% 81% 6% · 12%
1	B	262	83% · 14%
1	C	262	4% 85% · 13%
1	D	262	2% 81% 5% 14%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	C5S	B	302	-	X	-	-
5	C5S	D	302	-	X	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8237 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Putative amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	11	0
			1847	1154	328	351	14			
1	B	226	Total	C	N	O	S	0	6	0
			1783	1119	315	335	14			
1	C	229	Total	C	N	O	S	0	5	0
			1797	1127	316	340	14			
1	D	226	Total	C	N	O	S	0	4	0
			1762	1105	312	331	14			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q1M7F4
A	-18	GLY	-	expression tag	UNP Q1M7F4
A	-17	SER	-	expression tag	UNP Q1M7F4
A	-16	SER	-	expression tag	UNP Q1M7F4
A	-15	HIS	-	expression tag	UNP Q1M7F4
A	-14	HIS	-	expression tag	UNP Q1M7F4
A	-13	HIS	-	expression tag	UNP Q1M7F4
A	-12	HIS	-	expression tag	UNP Q1M7F4
A	-11	HIS	-	expression tag	UNP Q1M7F4
A	-10	HIS	-	expression tag	UNP Q1M7F4
A	-9	SER	-	expression tag	UNP Q1M7F4
A	-8	SER	-	expression tag	UNP Q1M7F4
A	-7	GLY	-	expression tag	UNP Q1M7F4
A	-6	LEU	-	expression tag	UNP Q1M7F4
A	-5	VAL	-	expression tag	UNP Q1M7F4
A	-4	PRO	-	expression tag	UNP Q1M7F4
A	-3	ARG	-	expression tag	UNP Q1M7F4
A	-2	GLY	-	expression tag	UNP Q1M7F4
A	-1	SER	-	expression tag	UNP Q1M7F4
A	0	HIS	-	expression tag	UNP Q1M7F4
A	142	ALA	LYS	conflict	UNP Q1M7F4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	234	GLY	-	expression tag	UNP Q1M7F4
A	235	LEU	-	expression tag	UNP Q1M7F4
A	236	VAL	-	expression tag	UNP Q1M7F4
A	237	PRO	-	expression tag	UNP Q1M7F4
A	238	ARG	-	expression tag	UNP Q1M7F4
A	239	GLY	-	expression tag	UNP Q1M7F4
A	240	SER	-	expression tag	UNP Q1M7F4
A	241	ILE	-	expression tag	UNP Q1M7F4
A	242	GLU	-	expression tag	UNP Q1M7F4
B	-19	MET	-	initiating methionine	UNP Q1M7F4
B	-18	GLY	-	expression tag	UNP Q1M7F4
B	-17	SER	-	expression tag	UNP Q1M7F4
B	-16	SER	-	expression tag	UNP Q1M7F4
B	-15	HIS	-	expression tag	UNP Q1M7F4
B	-14	HIS	-	expression tag	UNP Q1M7F4
B	-13	HIS	-	expression tag	UNP Q1M7F4
B	-12	HIS	-	expression tag	UNP Q1M7F4
B	-11	HIS	-	expression tag	UNP Q1M7F4
B	-10	HIS	-	expression tag	UNP Q1M7F4
B	-9	SER	-	expression tag	UNP Q1M7F4
B	-8	SER	-	expression tag	UNP Q1M7F4
B	-7	GLY	-	expression tag	UNP Q1M7F4
B	-6	LEU	-	expression tag	UNP Q1M7F4
B	-5	VAL	-	expression tag	UNP Q1M7F4
B	-4	PRO	-	expression tag	UNP Q1M7F4
B	-3	ARG	-	expression tag	UNP Q1M7F4
B	-2	GLY	-	expression tag	UNP Q1M7F4
B	-1	SER	-	expression tag	UNP Q1M7F4
B	0	HIS	-	expression tag	UNP Q1M7F4
B	142	ALA	LYS	conflict	UNP Q1M7F4
B	234	GLY	-	expression tag	UNP Q1M7F4
B	235	LEU	-	expression tag	UNP Q1M7F4
B	236	VAL	-	expression tag	UNP Q1M7F4
B	237	PRO	-	expression tag	UNP Q1M7F4
B	238	ARG	-	expression tag	UNP Q1M7F4
B	239	GLY	-	expression tag	UNP Q1M7F4
B	240	SER	-	expression tag	UNP Q1M7F4
B	241	ILE	-	expression tag	UNP Q1M7F4
B	242	GLU	-	expression tag	UNP Q1M7F4
C	-19	MET	-	initiating methionine	UNP Q1M7F4
C	-18	GLY	-	expression tag	UNP Q1M7F4
C	-17	SER	-	expression tag	UNP Q1M7F4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	SER	-	expression tag	UNP Q1M7F4
C	-15	HIS	-	expression tag	UNP Q1M7F4
C	-14	HIS	-	expression tag	UNP Q1M7F4
C	-13	HIS	-	expression tag	UNP Q1M7F4
C	-12	HIS	-	expression tag	UNP Q1M7F4
C	-11	HIS	-	expression tag	UNP Q1M7F4
C	-10	HIS	-	expression tag	UNP Q1M7F4
C	-9	SER	-	expression tag	UNP Q1M7F4
C	-8	SER	-	expression tag	UNP Q1M7F4
C	-7	GLY	-	expression tag	UNP Q1M7F4
C	-6	LEU	-	expression tag	UNP Q1M7F4
C	-5	VAL	-	expression tag	UNP Q1M7F4
C	-4	PRO	-	expression tag	UNP Q1M7F4
C	-3	ARG	-	expression tag	UNP Q1M7F4
C	-2	GLY	-	expression tag	UNP Q1M7F4
C	-1	SER	-	expression tag	UNP Q1M7F4
C	0	HIS	-	expression tag	UNP Q1M7F4
C	142	ALA	LYS	conflict	UNP Q1M7F4
C	234	GLY	-	expression tag	UNP Q1M7F4
C	235	LEU	-	expression tag	UNP Q1M7F4
C	236	VAL	-	expression tag	UNP Q1M7F4
C	237	PRO	-	expression tag	UNP Q1M7F4
C	238	ARG	-	expression tag	UNP Q1M7F4
C	239	GLY	-	expression tag	UNP Q1M7F4
C	240	SER	-	expression tag	UNP Q1M7F4
C	241	ILE	-	expression tag	UNP Q1M7F4
C	242	GLU	-	expression tag	UNP Q1M7F4
D	-19	MET	-	initiating methionine	UNP Q1M7F4
D	-18	GLY	-	expression tag	UNP Q1M7F4
D	-17	SER	-	expression tag	UNP Q1M7F4
D	-16	SER	-	expression tag	UNP Q1M7F4
D	-15	HIS	-	expression tag	UNP Q1M7F4
D	-14	HIS	-	expression tag	UNP Q1M7F4
D	-13	HIS	-	expression tag	UNP Q1M7F4
D	-12	HIS	-	expression tag	UNP Q1M7F4
D	-11	HIS	-	expression tag	UNP Q1M7F4
D	-10	HIS	-	expression tag	UNP Q1M7F4
D	-9	SER	-	expression tag	UNP Q1M7F4
D	-8	SER	-	expression tag	UNP Q1M7F4
D	-7	GLY	-	expression tag	UNP Q1M7F4
D	-6	LEU	-	expression tag	UNP Q1M7F4
D	-5	VAL	-	expression tag	UNP Q1M7F4

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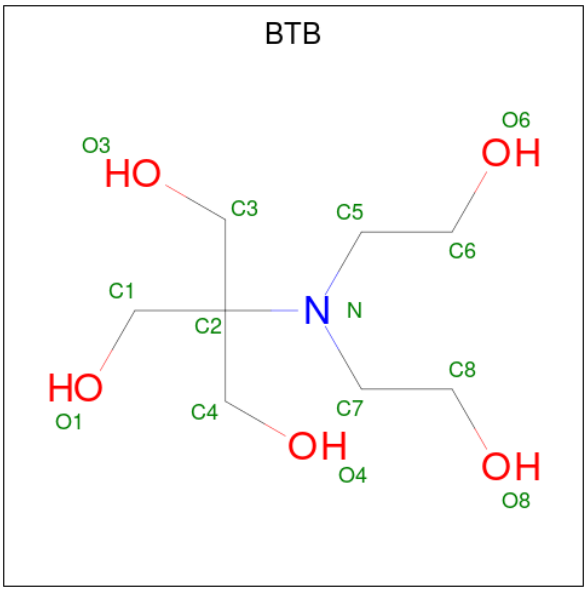
Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	PRO	-	expression tag	UNP Q1M7F4
D	-3	ARG	-	expression tag	UNP Q1M7F4
D	-2	GLY	-	expression tag	UNP Q1M7F4
D	-1	SER	-	expression tag	UNP Q1M7F4
D	0	HIS	-	expression tag	UNP Q1M7F4
D	142	ALA	LYS	conflict	UNP Q1M7F4
D	234	GLY	-	expression tag	UNP Q1M7F4
D	235	LEU	-	expression tag	UNP Q1M7F4
D	236	VAL	-	expression tag	UNP Q1M7F4
D	237	PRO	-	expression tag	UNP Q1M7F4
D	238	ARG	-	expression tag	UNP Q1M7F4
D	239	GLY	-	expression tag	UNP Q1M7F4
D	240	SER	-	expression tag	UNP Q1M7F4
D	241	ILE	-	expression tag	UNP Q1M7F4
D	242	GLU	-	expression tag	UNP Q1M7F4

- Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	1
			28	16	2	10		
2	B	1	Total	C	N	O	0	1
			28	16	2	10		
2	C	1	Total	C	N	O	0	1
			28	16	2	10		

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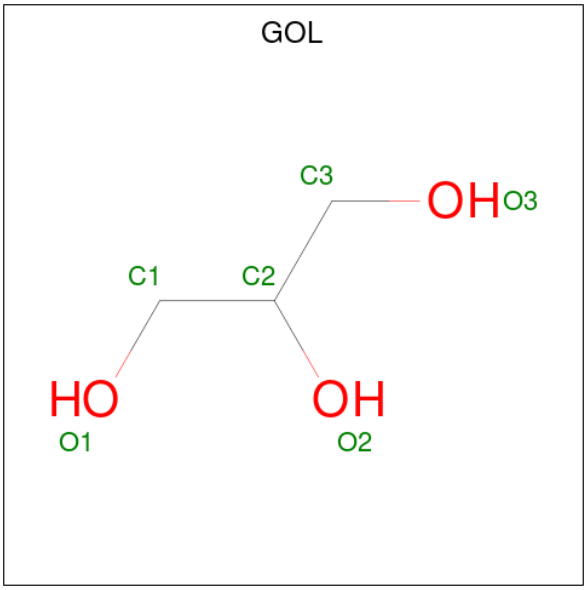
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	N	O	0	1
			28	16	2	10		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

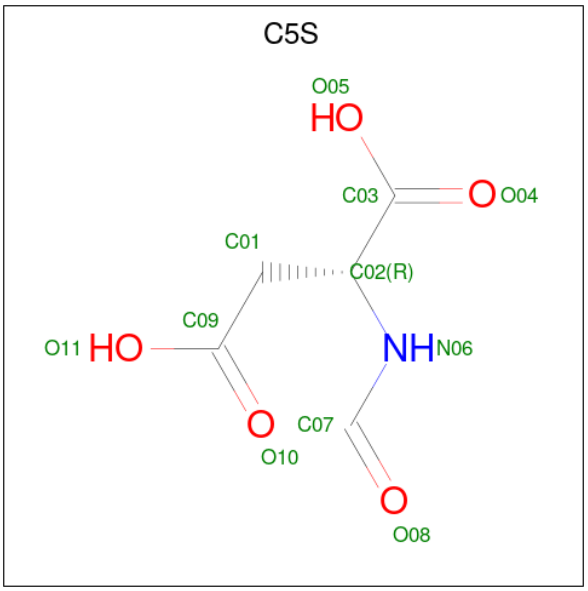


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

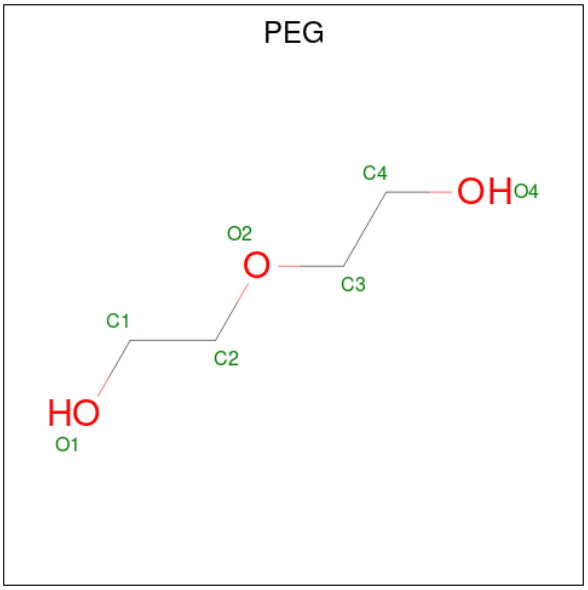
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is N-formyl-D-aspartic acid (three-letter code: C5S) (formula: $C_5H_7NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			11	5	1	5		
5	D	1	Total	C	N	O	0	0
			11	5	1	5		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is water.

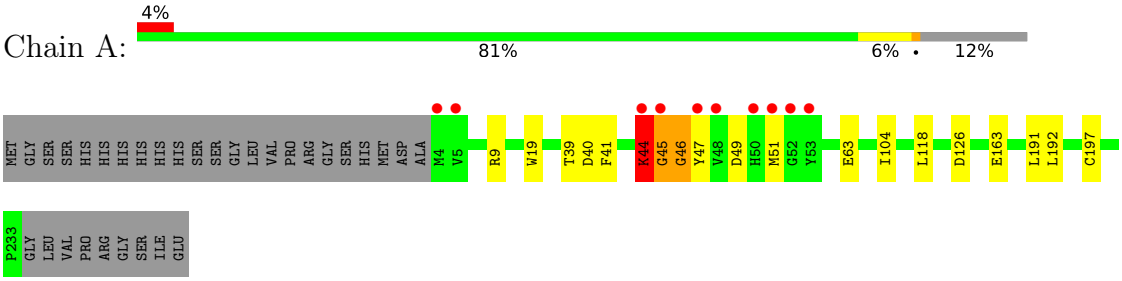
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	234	Total O 234 234	0	0
7	B	249	Total O 249 249	0	0
7	C	193	Total O 193 193	0	0
7	D	212	Total O 212 212	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

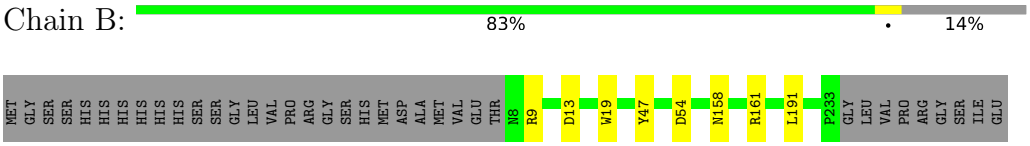
• Molecule 1: Putative amidase

Chain A:



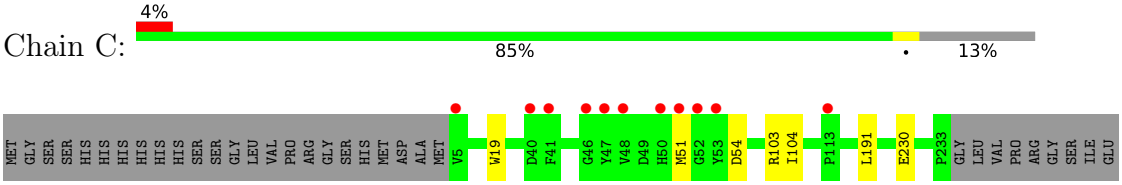
• Molecule 1: Putative amidase

Chain B:



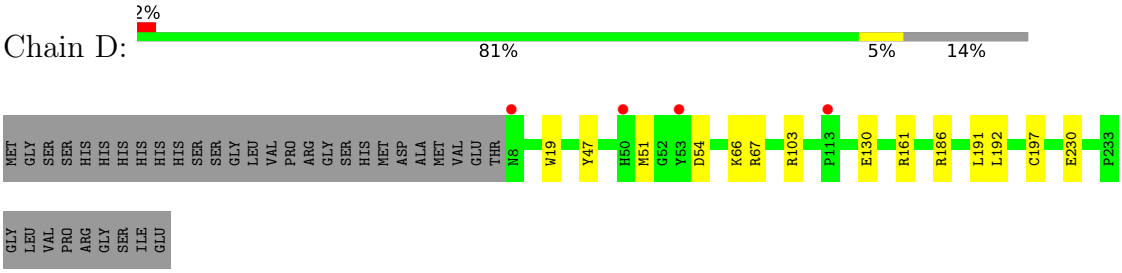
• Molecule 1: Putative amidase

Chain C:



• Molecule 1: Putative amidase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	62.07Å 122.24Å 136.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.90 – 1.59 43.55 – 1.59	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.90-1.59) 100.0 (43.55-1.59)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.54 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.154 , 0.174 0.167 , 0.184	Depositor DCC
R_{free} test set	6861 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	15.0	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	8237	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BTB, GOL, C5S, PEG, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.83	2/1886 (0.1%)	0.94	4/2560 (0.2%)
1	B	0.77	0/1821	0.89	3/2471 (0.1%)
1	C	0.75	0/1835	0.92	5/2492 (0.2%)
1	D	0.74	0/1800	0.91	6/2444 (0.2%)
All	All	0.78	2/7342 (0.0%)	0.91	18/9967 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46[A]	GLY	C-O	-6.70	1.12	1.23
1	A	46[B]	GLY	C-O	-6.70	1.12	1.23

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	103[A]	ARG	NE-CZ-NH1	6.91	123.76	120.30
1	C	103[B]	ARG	NE-CZ-NH1	6.91	123.76	120.30
1	B	54	ASP	CB-CG-OD2	-6.55	112.40	118.30
1	D	54	ASP	CB-CG-OD2	-6.27	112.66	118.30
1	B	13	ASP	CB-CG-OD2	-6.19	112.73	118.30
1	C	103[A]	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	C	103[B]	ARG	NE-CZ-NH2	-6.18	117.21	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	67	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	A	44	LYS	N-CA-C	5.80	126.66	111.00
1	B	9	ARG	NE-CZ-NH2	5.47	123.04	120.30
1	A	46[A]	GLY	C-N-CA	5.36	135.09	121.70
1	A	46[B]	GLY	C-N-CA	5.36	135.09	121.70
1	A	126	ASP	CB-CG-OD1	5.28	123.05	118.30
1	D	103[A]	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	D	103[B]	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	D	186	ARG	NE-CZ-NH1	-5.07	117.76	120.30
1	D	161	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	C	54	ASP	CB-CG-OD1	5.03	122.83	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	44	LYS	Mainchain
1	A	45[B]	GLY	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1847	0	1792	17	0
1	B	1783	0	1756	3	0
1	C	1797	0	1767	3	0
1	D	1762	0	1730	3	0
2	A	28	0	38	3	0
2	B	28	0	38	5	0
2	C	28	0	38	8	0
2	D	28	0	38	9	0
3	A	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	1	0	0	0	0
5	B	11	0	0	0	0
5	D	11	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	7	0	10	0	0
7	A	234	0	0	1	0
7	B	249	0	0	0	0
7	C	193	0	0	0	0
7	D	212	0	0	1	0
All	All	8237	0	7231	49	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (49) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40[B]:ASP:OD1	1:A:46[B]:GLY:HA3	1.50	1.09
2:B:301[B]:BTB:O8	2:B:301[B]:BTB:H51	1.55	1.02
2:A:301[B]:BTB:H71	2:A:301[B]:BTB:O6	1.57	0.99
2:D:301[B]:BTB:H51	2:D:301[B]:BTB:O8	1.67	0.95
2:C:301[A]:BTB:H71	2:C:301[A]:BTB:O4	1.77	0.84
1:A:41[B]:PHE:CZ	1:A:118:LEU:HD21	2.18	0.79
2:C:301[A]:BTB:H72	2:C:301[A]:BTB:O6	1.88	0.74
1:A:40[B]:ASP:OD1	1:A:46[B]:GLY:CA	2.33	0.74
5:D:302:C5S:O05	7:D:401:HOH:O	2.05	0.73
2:C:301[A]:BTB:O4	2:C:301[A]:BTB:C7	2.38	0.70
2:B:301[B]:BTB:O8	2:B:301[B]:BTB:C5	2.37	0.68
2:C:301[B]:BTB:O4	2:C:301[B]:BTB:C7	2.42	0.68
1:C:51:MET:SD	1:C:104:ILE:HD12	2.38	0.64
2:D:301[B]:BTB:O8	2:D:301[B]:BTB:C5	2.45	0.61
1:A:41[B]:PHE:HZ	1:A:118:LEU:HD21	1.68	0.59
2:C:301[B]:BTB:O4	2:C:301[B]:BTB:H71	2.03	0.58
1:A:163[B]:GLU:OE2	1:B:161:ARG:NH1	2.42	0.53
1:A:39:THR:O	1:A:40[B]:ASP:C	2.47	0.53
1:A:45[B]:GLY:O	1:A:49[B]:ASP:HB3	2.09	0.52
1:C:51:MET:SD	1:C:104:ILE:CD1	3.00	0.49
1:A:51:MET:SD	1:A:104:ILE:CD1	3.03	0.47
1:A:9[B]:ARG:CZ	7:A:445:HOH:O	2.63	0.47
1:C:19:TRP:CE2	1:C:191:LEU:HB2	2.50	0.47
2:C:301[B]:BTB:H71	2:C:301[B]:BTB:H12	1.69	0.47
2:D:301[A]:BTB:C5	2:D:301[A]:BTB:O3	2.63	0.47
1:A:19:TRP:CE2	1:A:191:LEU:HB2	2.50	0.47
2:B:301[B]:BTB:H72	2:B:301[B]:BTB:H31	1.66	0.46
1:B:19:TRP:CE2	1:B:191:LEU:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:301[A]:BTB:H62	2:D:301[A]:BTB:H61	1.96	0.46
2:B:301[A]:BTB:H52	2:B:301[A]:BTB:H11	1.63	0.46
1:A:40[A]:ASP:HA	1:A:46[A]:GLY:HA3	1.99	0.45
1:A:41[B]:PHE:HE1	1:A:47:TYR:CD2	2.34	0.45
1:D:19:TRP:CE2	1:D:191:LEU:HB2	2.51	0.45
2:D:301[B]:BTB:O3	2:D:301[B]:BTB:H52	2.16	0.45
1:A:51:MET:SD	1:A:104:ILE:HD12	2.56	0.44
1:D:66[B]:LYS:HE2	1:D:130:GLU:HB3	1.98	0.44
1:A:41[B]:PHE:CE1	1:A:47:TYR:HD2	2.35	0.44
2:A:301[A]:BTB:H11	2:A:301[A]:BTB:H51	1.85	0.43
2:A:301[A]:BTB:H82	1:B:158:ASN:O	2.17	0.43
1:A:40[B]:ASP:CG	1:A:46[B]:GLY:HA3	2.31	0.43
2:D:301[B]:BTB:C5	2:D:301[B]:BTB:O3	2.67	0.42
2:D:301[B]:BTB:H31	2:D:301[B]:BTB:H72	1.85	0.42
2:D:301[A]:BTB:O3	2:D:301[A]:BTB:H52	2.20	0.41
1:D:192:LEU:HD11	1:D:197[A]:CYS:SG	2.60	0.41
1:A:192:LEU:HD11	1:A:197[A]:CYS:SG	2.61	0.41
2:B:301[B]:BTB:C5	2:B:301[B]:BTB:O3	2.69	0.41
2:D:301[A]:BTB:H52	2:D:301[A]:BTB:H11	1.75	0.41
2:C:301[A]:BTB:H42	2:C:301[A]:BTB:H51	1.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	239/262 (91%)	232 (97%)	6 (2%)	1 (0%)	34 15
1	B	230/262 (88%)	226 (98%)	4 (2%)	0	100 100
1	C	232/262 (88%)	228 (98%)	4 (2%)	0	100 100
1	D	228/262 (87%)	224 (98%)	4 (2%)	0	100 100
All	All	929/1048 (89%)	910 (98%)	18 (2%)	1 (0%)	51 29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	LYS

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/213 (91%)	193 (100%)	1 (0%)	88	80
1	B	189/213 (89%)	188 (100%)	1 (0%)	88	80
1	C	191/213 (90%)	190 (100%)	1 (0%)	88	80
1	D	186/213 (87%)	183 (98%)	3 (2%)	62	41
All	All	760/852 (89%)	754 (99%)	6 (1%)	81	70

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	GLU
1	B	47	TYR
1	C	230	GLU
1	D	47	TYR
1	D	51	MET
1	D	230	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	C5S	B	302	1	10,10,10	4.06	6 (60%)	11,12,12	3.82	6 (54%)
2	BTB	A	301[A]	-	13,13,13	0.55	0	7,16,16	0.47	0
2	BTB	B	301[B]	-	13,13,13	0.67	0	7,16,16	0.59	0
2	BTB	D	301[A]	-	13,13,13	0.69	0	7,16,16	0.89	0
3	GOL	C	302	-	5,5,5	0.99	0	5,5,5	0.50	0
3	GOL	D	304	-	5,5,5	0.54	0	5,5,5	0.52	0
5	C5S	D	302	1	10,10,10	3.61	5 (50%)	11,12,12	3.46	9 (81%)
3	GOL	A	302	-	5,5,5	0.86	0	5,5,5	0.65	0
2	BTB	C	301[B]	-	13,13,13	0.65	0	7,16,16	0.96	0
6	PEG	D	303	-	6,6,6	0.38	0	5,5,5	0.54	0
2	BTB	A	301[B]	-	13,13,13	0.70	0	7,16,16	0.93	0
2	BTB	B	301[A]	-	13,13,13	0.77	0	7,16,16	1.08	1 (14%)
2	BTB	C	301[A]	-	13,13,13	0.74	0	7,16,16	0.71	0
2	BTB	D	301[B]	-	13,13,13	0.63	0	7,16,16	0.46	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	C5S	B	302	1	-	4/11/11/11	-
2	BTB	A	301[A]	-	-	1/21/21/21	-
2	BTB	B	301[B]	-	-	1/21/21/21	-
2	BTB	D	301[A]	-	-	1/21/21/21	-
3	GOL	C	302	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	304	-	-	0/4/4/4	-
5	C5S	D	302	1	-	4/11/11/11	-
3	GOL	A	302	-	-	0/4/4/4	-
2	BTB	C	301[B]	-	-	1/21/21/21	-
6	PEG	D	303	-	-	2/4/4/4	-
2	BTB	A	301[B]	-	-	1/21/21/21	-
2	BTB	B	301[A]	-	-	1/21/21/21	-
2	BTB	C	301[A]	-	-	2/21/21/21	-
2	BTB	D	301[B]	-	-	2/21/21/21	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	302	C5S	C02-N06	9.09	1.58	1.45
5	D	302	C5S	C02-N06	7.58	1.56	1.45
5	D	302	C5S	C07-N06	6.90	1.56	1.33
5	B	302	C5S	C07-N06	6.32	1.54	1.33
5	B	302	C5S	O05-C03	-3.82	1.18	1.30
5	B	302	C5S	C01-C02	3.56	1.61	1.53
5	D	302	C5S	O04-C03	-2.58	1.14	1.22
5	B	302	C5S	O10-C09	2.33	1.29	1.22
5	D	302	C5S	O10-C09	2.33	1.29	1.22
5	B	302	C5S	O04-C03	2.19	1.28	1.22
5	D	302	C5S	C01-C02	2.04	1.58	1.53

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	302	C5S	C02-N06-C07	6.95	133.51	122.82
5	B	302	C5S	C02-C01-C09	5.77	129.72	112.88
5	D	302	C5S	C02-N06-C07	5.51	131.30	122.82
5	B	302	C5S	O08-C07-N06	-5.41	111.03	125.27
5	D	302	C5S	O08-C07-N06	-4.93	112.28	125.27
5	B	302	C5S	C03-C02-N06	-4.69	99.48	110.55
5	D	302	C5S	C02-C01-C09	4.10	124.86	112.88
5	D	302	C5S	O05-C03-O04	-3.78	115.50	124.09
5	B	302	C5S	O11-C09-O10	-3.49	114.61	123.30
5	D	302	C5S	O11-C09-C01	3.38	124.91	114.07
5	D	302	C5S	C03-C02-N06	-3.10	103.23	110.55
5	D	302	C5S	O11-C09-O10	-3.08	115.62	123.30
5	B	302	C5S	C01-C02-C03	-2.98	105.07	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	302	C5S	O05-C03-C02	2.92	123.12	113.40
2	B	301[A]	BTB	O4-C4-C2	-2.37	104.94	111.44
5	D	302	C5S	C01-C02-C03	-2.25	106.48	110.83

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301[B]	BTB	C8-C7-N-C5
2	C	301[A]	BTB	C6-C5-N-C7
2	D	301[B]	BTB	C8-C7-N-C5
5	D	302	C5S	C03-C02-N06-C07
2	A	301[A]	BTB	N-C7-C8-O8
6	D	303	PEG	O2-C3-C4-O4
2	C	301[A]	BTB	N-C7-C8-O8
2	C	301[B]	BTB	N-C7-C8-O8
2	D	301[A]	BTB	N-C5-C6-O6
2	B	301[A]	BTB	N-C5-C6-O6
2	D	301[B]	BTB	N-C5-C6-O6
5	B	302	C5S	N06-C02-C03-O04
5	B	302	C5S	N06-C02-C03-O05
5	D	302	C5S	N06-C02-C03-O04
5	B	302	C5S	C01-C02-C03-O05
6	D	303	PEG	C1-C2-O2-C3
5	D	302	C5S	C01-C02-C03-O04
5	B	302	C5S	C01-C02-C03-O04
2	A	301[B]	BTB	C8-C7-N-C5
5	D	302	C5S	C01-C02-C03-O05

There are no ring outliers.

9 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301[A]	BTB	2	0
2	B	301[B]	BTB	4	0
2	D	301[A]	BTB	4	0
5	D	302	C5S	1	0
2	C	301[B]	BTB	3	0
2	A	301[B]	BTB	1	0
2	B	301[A]	BTB	1	0
2	C	301[A]	BTB	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301[B]	BTB	5	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	230/262 (87%)	-0.06	10 (4%) 35 32	9, 14, 29, 50	0
1	B	226/262 (86%)	-0.34	0 100 100	10, 13, 22, 40	0
1	C	229/262 (87%)	-0.01	11 (4%) 30 28	9, 15, 29, 42	0
1	D	226/262 (86%)	-0.20	4 (1%) 68 67	9, 15, 30, 46	0
All	All	911/1048 (86%)	-0.15	25 (2%) 54 52	9, 14, 29, 50	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	48	VAL	8.0
1	A	48	VAL	6.6
1	A	47	TYR	5.2
1	A	4	MET	5.1
1	A	50	HIS	4.9
1	A	53	TYR	4.3
1	A	5	VAL	4.1
1	C	50	HIS	3.6
1	A	51	MET	3.3
1	A	52	GLY	3.2
1	C	5	VAL	3.2
1	C	53	TYR	3.2
1	C	47	TYR	3.1
1	C	51	MET	3.1
1	C	41	PHE	2.9
1	D	8	ASN	2.9
1	C	40	ASP	2.7
1	D	50	HIS	2.7
1	C	52	GLY	2.4
1	D	53	TYR	2.4
1	A	44	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	113	PRO	2.3
1	D	113	PRO	2.2
1	A	45[A]	GLY	2.1
1	C	46	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	C5S	D	302	11/11	0.84	0.23	12,29,40,41	11
5	C5S	B	302	11/11	0.86	0.21	14,28,40,50	0
6	PEG	D	303	7/7	0.88	0.10	35,36,39,39	7
3	GOL	A	302	6/6	0.89	0.18	15,21,25,25	6
3	GOL	C	302	6/6	0.90	0.17	16,24,25,28	0
2	BTB	C	301[B]	14/14	0.91	0.12	17,19,26,29	14
2	BTB	C	301[A]	14/14	0.91	0.12	14,17,22,25	14
2	BTB	D	301[A]	14/14	0.92	0.11	12,14,20,24	14
2	BTB	D	301[B]	14/14	0.92	0.11	21,23,31,36	14
4	CL	A	303	1/1	0.92	0.09	46,46,46,46	0
2	BTB	B	301[A]	14/14	0.93	0.11	12,14,18,21	14
2	BTB	B	301[B]	14/14	0.93	0.11	25,26,33,38	14
2	BTB	A	301[B]	14/14	0.94	0.11	18,20,28,34	14
3	GOL	D	304	6/6	0.94	0.14	16,24,28,29	0
2	BTB	A	301[A]	14/14	0.94	0.11	13,14,17,18	14

6.5 Other polymers (i)

There are no such residues in this entry.